Amendments to the Specification:

Please replace the paragraph beginning at page 13, line 26, with the following redlined paragraph:

-- DSP-16 polynucleotides may comprise a native sequence (*i.e.*, an endogenous DSP-16 or DSP-16 alternate form sequence, or a portion or splice variant thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the activity of the encoded polypeptide is not substantially diminished, as described above. The effect on the activity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native DSP-16 or DSP-16 alternate form or a portion thereof. The percent identity may be readily determined by comparing sequences using computer algorithms well known to those having ordinary skill in the art, such as Align or the BLAST algorithm (Altschul, *J. Mol. Biol. 219*:555-565, 1991; Henikoff and Henikoff, *Proc. Natl. Acad. Sci. USA 89*:10915-10919, 1992), which is available at the NCBI website (retrieved from the Internet:URL: ~~http://~~www/ncbi.nlm.nih.gov/cgi-bin/BLAST). Default parameters may be used. Certain variants are substantially homologous to a native gene. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA or RNA sequence encoding a native DSP-16 or DSP-16 alternate form (or a complementary sequence). Suitable moderately stringent conditions include, for example, prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-70°C, 5 X SSC, for 1-16 hours (*e.g.*, overnight); followed by washing once or twice at 22-65°C for 20-40 minutes with one or more each of 2X, 0.5X and 0.2X SSC containing 0.05-0.1% SDS. For additional stringency, conditions may include a wash in 0.1X SSC and 0.1% SDS at 50-60 °C for 15-40 minutes. As known to those having ordinary skill in the art, variations in stringency of hybridization conditions may be achieved by altering the time, temperature and/or concentration of the solutions used for prehybridization, hybridization and wash steps, and suitable conditions may also depend in part on the particular nucleotide

sequences of the probe used, and of the blotted, proband nucleic acid sample. Accordingly, it will be appreciated that suitably stringent conditions can be readily selected without undue experimentation where a desired selectivity of the probe is identified, based on its ability to hybridize to one or more certain proband sequences while not hybridizing to certain other proband sequences.--

Please replace the paragraph beginning at page 16, line 10, with the following redlined paragraph:

-- A cDNA sequence encoding DSP-16 is provided in Figure 1 (SEQ ID NO:1), and the predicted amino acid sequence is provided in Figure 2 (SEQ ID NO:2). A cDNA sequence encoding a DSP-16 alternate form is provided in Figure 3 (SEQ ID NO:20), and the predicted amino acid sequence, which includes the DSP-16 active site VHCLAGISRS (SEQ ID NO:16), is provided in Figure 4 (SEQ ID NO:21). Sequence information immediately adjacent to this site was used to design 5' and 3' RACE reactions with human thymus or human brain, skeletal muscle and testis cDNA to identify a protein of 665 amino acids (Fig. 2) encoded by 1995 base pairs. This protein is referred to as dual specificity phosphatase-~~3~~16, or DSP-16. This approach also permitted identification of a DSP-16 alternate form protein of 517 amino acids (Fig. 4) encoded by 1551 base pairs which, according to non-limiting theory, may be the product of alternate splicing at the polynucleotide level. DSP-16 shows significant homology to other MAP-kinase phosphatases, as shown by the sequence comparison presented in Figure 5. --

Please replace the paragraph beginning at page 50, line 16, with the following redlined paragraph:

-- To derive a longer consensus DSP amino acid sequence motif that would be useful for the identification of new DSP family members, multiple known human dual-specificity phosphatases sequences were aligned and compared. An alignment of eight amino acid sequences derived from eight human DSPs having MAP-kinase phosphatase activity yielded

a conserved homology region consisting of a 24-amino acid peptide sequence containing the PTP active site signature motif. Thus, a candidate peptide having the sequence:

NGRVLVHCQAGISRSGTNILAYLM SEQ ID NO:17

was used to search the "month" database (Nat. Center for Biol. Information, retrieved from the Internet:URL:www.ncbi.nlm.nih.gov/blast.cgi?Jform=1). The search employed an algorithm (tblastn) capable of reverse translation of the candidate peptide with iterations allowing for genetic code degeneracy within default parameters. --

Please replace the paragraph beginning at page 51, line 17, with the following redlined paragraph:

-- Resubmission of AW461438 as a query sequence to the GenBank "nr" (nonredundant) database revealed alignment of the query sequence with the putative exon regions of AC007619. The alignment of AC007619 with AW461438 was then used to derive portions of AC007619 comprising a theoretical human DSP cDNA sequence, by aligning regions of AW461438 with three presumptive exon regions of AC007619 and identifying classical splice junction (donor/acceptor) sites in AC007619. AW461438 exhibited greater than 90% homology with the exon regions of AC007619 by this alignment. This theoretical human DSP cDNA sequence was then used as a blastn query in the GenBank "dbest" database (retrieved from the Internet:URL:www.ncbi.nlm.nih.gov/dbest). The human EST AW847425 was identified by this search; the 3' end of the reverse complement of AW847425 contained a 130 nucleotide overlap with the theoretical human DSP cDNA sequence. AW847425 also contained additional putative exon regions that were present in AC007619. A concensus sequence was deduced from the alignment of AW847425 with the theoretical human DSP cDNA sequence identified as described above (*i.e.*, by alignment of AC007619 and AW461438). Analysis of the deduced consensus sequence showed the presence of six exons with only three nucleotides mismatched. Where there was a mismatch, the nucleotide situated at the corresponding position in AC007619

was used to arrive at the consensus sequence. From this concensus sequence, the following PCR primers were designed:

PCR—5':

CAA AGT GTT AAT TAC AGA GCT CAT CCA GCA TTC AGC GA—3'

SEQ ID NO: 14

PCR—3':

5'—TTG GCT TCT CCA GGT GCA GCA GCT TGA GTT—3' SEQ ID NO: 15 --